

FILE 'HOME' ENTERED AT 15:39:37 ON 21 SEP 2006

=> file medline biosis caplus

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

0.21

0.21

FILE 'MEDLINE' ENTERED AT 15:40:05 ON 21 SEP 2006

FILE 'BIOSIS' ENTERED AT 15:40:05 ON 21 SEP 2006

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FILE 'CAPLUS' ENTERED AT 15:40:05 ON 21 SEP 2006

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.

PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

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=> opioid or opiate

L1 166446 OPIOID OR OPIATE

=> substance p

L2 63250 SUBSTANCE P

=> l1 and l2

L3 2774 L1 AND L2

=> chimera? or fusion

L4 605910 CHIMER? OR FUSION

=> l3 and l4

L5 27 L3 AND L4

=> dup rem l5

PROCESSING COMPLETED FOR L5

L6 17 DUP REM L5 (10 DUPLICATES REMOVED)

=> l6 and 1970-1998/py

L7 3 L6 AND 1970-1998/PY

=> daniel?/au and carr?/au

L8 235 DANIEL?/AU AND CARR?/AU

=> andrezej?/au and lipkowski?/au

L9 0 ANDREZEJ?/AU AND LIPKOWSKI?/AU

=> richard?/au and kream?/au

L10 11 RICHARD?/AU AND KREAM?/AU

=> aleksandra?/au and micicka-kesik?/au

L11 0 ALEKSANDRA?/AU AND MICICKA-KESIK?/AU

=> l8 or l10

L12 246 L8 OR L10

=> l7 and l12

L13 0 L7 AND L12

=> d ti abs so l7 1-3

L7 ANSWER 1 OF 3 MEDLINE on STN

TI ***Opioid*** and neurokinin activities of ***substance***

p fragments and their analogs.

AB Newly developed ***substance*** (SP) analogs with altered N-terminal sequences which equalize the lipophilicity of the N-terminal and C-terminal elements and of their ***fusion*** product were examined using i.t. injection in mice. I.t. injection of either the full length analog or the C-terminal hexapeptide (CP) produced biting and scratching behavior similar to that elicited by SP. SPF was approximately 5-fold and CP 14-fold less potent than native SP. The N-terminal peptide (NP) was inactive by itself but inhibited CP-elicited behavior. Naloxone

antagonized this action of NP and shifted the SPF dose-response curve 4-fold to the left. However, naloxone had no effect on the action of CP or on the action of any of the native neurokinins. The results are consistent with the hypothesis that N- and C-terminal analogs of SP can have ***opioid*** and SP-like actions, respectively, in the CNS of rodents. Furthermore, analogs of SP which include at least the terminal tetrapeptide retain neurokinin activity.

SO European journal of pharmacology, *** (1991 Feb 7) *** Vol. 193, No. 2, pp. 209-15.
Journal code: 1254354. ISSN: 0014-2999.

L7 ANSWER 2 OF 3 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI A novel synthetic ***chimeric*** analgesic molecule active upon
opioid and neurokinin receptors.
SO Anesthesiology (Hagerstown), (***Sept., 1998***) Vol. 89, No. 3A, pp. A1124. print.
Meeting Info.: Annual Meeting of the American Society of Anesthesiologists. Orlando, Florida, USA. October 17-21, 1998. American Society of Anesthesiologists.
CODEN: ANESAV. ISSN: 0003-3022.

L7 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2006 ACS on STN
TI Production of peptide or protein as ***fusion*** proteins
AB A ***fusion*** protein (markush structure given) contg. a carrier protein, .gtoreq.1 enzyme cleavable peptide sequences as linkers, and desired peptide in tandem repeat (markush structure given). Construction of expression plasmid pMD500R5 encoding a ***fusion*** protein of protein A-linkers-5 VIP units (vasoactive intestinal polypeptide) was shown. The plasmid was transformed into Bacillus subtilis SPL14 for fermn. of the ***fusion*** protein. Also shown was the prepn. of VIP from the ***fusion*** protein by incubation with basic amino acid-specific protease, blood coagulation factor Xa, and kallikrein.
SO PCT Int. Appl., 53 pp.
CODEN: PIXXD2

=> d his

(FILE 'HOME' ENTERED AT 15:39:37 ON 21 SEP 2006)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:40:05 ON 21 SEP 2006

L1 166446 OPIOID OR OPIATE
L2 63250 SUBSTANCE P
L3 2774 L1 AND L2
L4 605910 CHIMER? OR FUSION
L5 27 L3 AND L4
L6 17 DUP REM L5 (10 DUPLICATES REMOVED)
L7 3 L6 AND 1970-1998/PY
L8 235 DANIEL?/AU AND CARR?/AU
L9 0 ANDREZEJ?/AU AND LIPKOWSKI?/AU
L10 11 RICHARD?/AU AND KREAM?/AU
L11 0 ALEKSANDRA?/AU AND MICICKA-KESIK?/AU
L12 246 L8 OR L10
L13 0 L7 AND L12

=> .logoff

WEST Search History

DATE: Thursday, September 21, 2006

Hide? Set Name Query**Hit Count***DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=AND*

<input type="checkbox"/>	L15	l9 and L14	7
<input type="checkbox"/>	L14	l10 or l11 or l12 or L13	122
<input type="checkbox"/>	L13	aleksandra.in. and misicka-kesik.in.	2
<input type="checkbox"/>	L12	richard.in. and kream.in.	8
<input type="checkbox"/>	L11	andrzej.in. and lipkowski.in.	12
<input type="checkbox"/>	L10	daniel.in. and carr.in.	113
<input type="checkbox"/>	L9	opioid same substance same p same (chimera or chimeric or fusion)	18
<input type="checkbox"/>	L8	opioid same substance same p	760
<input type="checkbox"/>	L7	l4 and l6	573
<input type="checkbox"/>	L6	chimera or chimeric or fusion	275054
<input type="checkbox"/>	L5	chimera or chimeric or fusion	275054
<input type="checkbox"/>	L4	l2 and L3	1444
<input type="checkbox"/>	L3	substance adj p	8587
<input type="checkbox"/>	L2	opioid	10944

DB=USPT; PLUR=YES; OP=AND

<input type="checkbox"/>	L1	6759520	1
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END OF SEARCH HISTORY

SCORE Search Results Details for Application 10828623 and Search Result us-10-828-623c-21.rag.

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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:20:03 ; Search time 196 Seconds
(without alignments)
25.660 Million cell updates/sec

Title: US-10-828-623C-21
Perfect score: 61
Sequence: 1 RPKPQQFFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SCORE Search Results Details for Application 10828623 and Search Result us-10-828-623c-21

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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:38:02 ; Search time 46.5 Seconds
(without alignments)
20.706 Million cell updates/sec

Title: US-10-828-623C-21
Perfect score: 61
Sequence: 1 RPKPQQFFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	61	100.0	11	1 US-07-934-553-1	Sequence 1, Appli
2	61	100.0	11	1 US-08-184-935-12	Sequence 12, Appli

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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:38:07 ; Search time 155 Seconds
(without alignments)
32.873 Million cell updates/sec

Title: US-10-828-623C-21
Perfect score: 61
Sequence: 1 RPKPQQFFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	3	US-09-265-690C-3
					Sequence 3, Appli

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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:40:32 ; Search time 26.5 Seconds
(without alignments)
29.325 Million cell updates/sec

Title: US-10-828-623C-21
Perfect score: 61
Sequence: 1 RPKPQQFFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 256596 seqs, 70647373 residues

Total number of hits satisfying chosen parameters: 256596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:30:17 ; Search time 30 Seconds
(without alignments)
35.279 Million cell updates/sec

Title: US-10-828-623C-21
Perfect score: 61
Sequence: 1 RPKPQQFFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	61	100.0	11	1 A60654	substance P - guin
2	61	100.0	11	1 SPHO	substance P - hors
3	61	100.0	63	2 JC2412	tachykinin gamma c
4	61	100.0	72	2 JC5455	preprotachykinin-A
5	61	100.0	72	2 I62742	tachykinin A gamma
6	61	100.0	97	2 S12958	tachykinin delta p
7	61	100.0	112	1 SPRTA	substance P alpha
8	61	100.0	115	1 SPRBG	substance P gamma

SCORE Search Results Details for Application 10828623 and Search Result us-10-828-623c-21.rup.

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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:21:13 ; Search time 239.5 Seconds
(without alignments)
42.485 Million cell updates/sec

Title: US-10-828-623C-21
Perfect score: 61
Sequence: 1 RPKPQQFFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	61	100.0	11	1 TKNA_CAVPO	P67932 cavia porce
2	61	100.0	11	1 TKNA_HORSE	P67933 equus cabal
3	61	100.0	72	2 Q9Y494_HUMAN	Q9y494 homo sapien
4	61	100.0	96	2 Q549V0_HUMAN	Q549v0 homo sapien

SCORE Search Results Details for Application 10828623 and Search Result us-10-828-623c-3.rag.

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OM protein - protein search, using sw model

```
Run on:      September 13, 2006, 19:20:03 ; Search time 71.2727 Seconds
              (without alignments)
              25.660 Million cell updates/sec
```

```
Title:      US-10-828-623C-3
Perfect score: 26
Sequence:    1 YPFF 4
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      A_Geneseq_8:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SCORE Search Results Details for Application 10828623 and Search Result us-10-828-623c-3.ra1.

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OM protein - protein search, using sw model

```
Run on:          September 13, 2006, 19:38:02 ; Search time 16.9091 Seconds
                (without alignments)
                20.706 Million cell updates/sec
```

```
Title:      US-10-828-623C-3
Perfect score: 26
Sequence:   1 YPFF 4
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      Issued_Patents_AA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:38:07 ; Search time 56.3636 Seconds
(without alignments)
32.873 Million cell updates/sec

Title: US-10-828-623C-3
Perfect score: 26
Sequence: 1 YPFF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	26	100.0	4	3	US-09-994-078-1 Sequence 1, Appli

http://es/ScoreAccessWeb/GetItem.action?AppId=10828623&seqId=643601&ItemName=us... 9/21/06

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:30:17 ; Search time 10.9091 Seconds
(without alignments)
35.279 Million cell updates/sec

Title: US-10-828-623C-3
Perfect score: 26
Sequence: 1 YPFF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	50	2	A05031	hypothetical prote
2	26	100.0	79	2	S77831	hypothetical prote
3	26	100.0	84	2	T17637	hypothetical prote
4	26	100.0	103	2	T18203	mnxA protein - Bac
5	26	100.0	104	2	AG0706	probable membrane
6	26	100.0	106	2	H71127	hypothetical prote
7	26	100.0	108	2	T17630	hypothetical prote
8	26	100.0	115	2	D89103	protein C18B10.5 [

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OM protein - protein search, using sw model

```
Run on:      September 13, 2006, 19:21:13 ; Search time 87.0909 Seconds
              (without alignments)
              42.485 Million cell updates/sec
```

```
Title:      US-10-828-623C-3
Perfect score: 26
Sequence:   1 YPFF 4
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      UniProt_7.2:*
           1:  uniprot_sprot:*
           2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	26	100.0		17	2	Q7RTA3_PLAYO	Q7rta3 plasmodium
2	26	100.0		26	2	Q4YBW9_PLABE	Q4ybw9 plasmodium
3	26	100.0		27	2	Q7RDK6_PLAYO	Q7rdk6 plasmodium
4	26	100.0		30	2	Q81VH7_BACAN	Q81vh7 bacillus an

SCORE Search Results Details for Application 10828623 and Search Result us-10-828-623c- 42.rag.

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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:20:03 ; Search time 124.727 Seconds
(without alignments)
25.660 Million cell updates/sec

Title: US-10-828-623C-42
Perfect score: 41
Sequence: 1 YPFFGLM 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SCORE Search Results Details for Application 10828623 and Search Result us-10-828-623c-42

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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:38:02 ; Search time 29.5909 Seconds
(without alignments)
20.706 Million cell updates/sec

Title: US-10-828-623C-42
Perfect score: 41
Sequence: 1 YPFFGLM 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	41	100.0	7	2 US-09-428-692-42	Sequence 42, Appl
2	38	92.7	384	2 US-09-902-540-15078	Sequence 15078, A

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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:38:07 ; Search time 98.6364 Seconds
(without alignments)
32.873 Million cell updates/sec

Title: US-10-828-623C-42
Perfect score: 41
Sequence: 1 YPFFGLM 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	36	87.8	111	4 US-10-425-115-360665	Sequence 360665,
2	36	87.8	219	4 US-10-767-701-44311	Sequence 44311, A
3	36	87.8	242	4 US-10-767-701-44310	Sequence 44310, A

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OM protein - protein search, using sw model

Run on: September 13, 2006, 19:40:32 ; Search time 16.8636 Seconds
(without alignments)
29.325 Million cell updates/sec

Title: US-10-828-623C-42
Perfect score: 41
Sequence: 1 YPFFGLM 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 256596 seqs, 70647373 residues

Total number of hits satisfying chosen parameters: 256596

Minimum DB seq length: 0
Maximum DB seq length: 20000000000.

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query